

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

2032	20	Y00240	Enterococcus
2032	20	Y00242	Enterococcus
2032	7	Y02267	Collagen b
2032	13	Y02267	S. Pyogene
2032	13	Y02267	Staphylococcus
2032	20	Y08603	Staphylococcus
2032	20	W41602	Microplasmoma
2032	19	W63451	Cell wall
2032	19	W63451	Staph. epini
2032	21	Y03171	Enterococcus
2032	21	Y70120	Enterococcus
2032	20	Y02219	Enterococcus
2032	20	Y00211	C. difficile
2032	17	R95011	Clostridium
2032	19	W63388	Moraxella
2032	20	W89417	Photobacterium
2032	20	Y33729	Arabidopsis
2032	21	G30569	Arabidopsis
2032	21	G30569	Arabidopsis
2032	21	G30569	Arabidopsis
2032	21	G30569	Arabidopsis
2032	21	G30569	Arabidopsis
2032	21	G30569	Arabidopsis
2032	17	R77673	S-layer protein
2032	18	W22862	Bacillus
2032	20	W93252	B. stearothermophilus
2032	21	B10625	B. stearothermophilus
2032	21	B10625	Streptococcus
2032	18	W22863	Bacillus
2032	21	B10625	B. stearothermophilus
2032	12	R12083	HMP protein
2032	3	Y81266	Streptococcus
2032	21	Y81266	H. Pylori
2032	18	W20535	H. Pylori
2032	18	W21012	Bacteriophage
2032	18	W21012	Enterococcus
2032	12	Y1684	Streptococcus
2032	12	Y1684	Adhesion
2032	20	Y00243	Polypeptide
2032	21	Y81627	Y81627
2032	17	R92768	Y81627
2032	21	1394	Adhesion
2032	21	795	Polypeptide
2032	21	B03138	Polypeptide
ALIGNMENTS			
First entry			
Vhalis VH19 lactoferrin binding protein 2 (Lbp2).			
Lbp2; lactoferrin binding protein; lbp2; infection; otitis media; sinusitis; conjunctivitis; chritis; tracheitis; emphysema; diagnosis; therapy; melia catarrhalis.			
Lbp2; Protein; 905 AA.			
Location/Qualifiers			
282		/note= "encoded by GAC"	
283		/note= "encoded by TAT"	
284		/note= "encoded by GAG"	
285		/note= "encoded by GGC"	
286		/note= "encoded by AAT"	
287		/note= "encoded by TGC"	
288		/note= "encoded by TTG"	
290		/note= "encoded by CTC"	

FT	Misc-difference	291	/note= "encoded by ACC"	220	-----MRQALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----254
FT	Misc-difference	292	/note= "encoded by GAT"	221	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----255
FT	Misc-difference	293	/note= "encoded by GTC"	222	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----256
FT	Misc-difference	294	/note= "encoded by ARA"	223	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----257
FT	Misc-difference	296	/note= "encoded by CGC"	224	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----258
FT	Misc-difference	297	/note= "encoded by CCA"	225	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----259
FT	Misc-difference	298	/note= "encoded by TTT"	226	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----260
FT	Misc-difference	299	/note= "encoded by GAT"	227	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----261
FT	Region	435..441	/note= "conserved epitope"	228	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----262
PN	W09855606-A2.			229	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----263
XX	10-DEC-1998.			230	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----264
XX	98WO-CA00544.			231	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----265
PF	02-JUN-1998;			232	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----266
XX	08-MAY-1998;	98US-0074658.		233	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----267
PR	03-JUN-1997;	97US-0867941.		234	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----268
XX	(CONN-) CONNAUGHT LAB LTD.			235	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----269
PA	Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;			236	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----270
XX	DR	WPI: 1999-070266/06.		237	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----271
XX	N-PSDB; v82021.			238	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----272
PT	Lactoferrin receptor genes from <i>Moraxella</i> , especially <i>M. catarrhalis</i> - useful to diagnose <i>Moraxella</i> infection e.g. to detect otitis media due to <i>M. catarrhalis</i> infection and to immunise against such infections			239	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----273
PT	PI	Claim 8; Fig 16; 202pp; English.		240	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----274
XX	CC	This protein comprises lactoferrin binding protein 2 (lbp2) of <i>Moraxella catarrhalis</i> (Brannhamella catarrhalis) VH9. It is encoded by the lbp2 gene of the lactoferrin receptor (lfr) locus (see V2021) identified in the <i>M. catarrhalis</i> VH9 genome.		241	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----275
CC	CC	Immunogenic compositions, including vaccines, based upon expressed recombinant lbp1 and/or lbp2 and/or ORF3 proteins (see W89413-21), portions of these, or their analogues, can be prepared for prevention of diseases caused by <i>Moraxella</i> . <i>M. catarrhalis</i> is a causative agent of otitis media and has been associated with sinusitis, conjunctivitis and inflammatory diseases of the lower respiratory tract, such as pneumonia, chronic bronchitis, tracheitis and emphysema.		242	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----276
XX	CC	CC	CC	243	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----277
SQ	Sequence	905 AA;		244	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----278
RESULT	2			245	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----279
Y90257				246	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----280
ID	Y90257	standard; Protein; 597 AA.		247	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----281
XX				248	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----282
AC	Y90257;			249	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----283
XX				250	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----284
DT	19-SEP-2000	(first entry)		251	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----285
XX				252	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----286
DE	Streptococcus equi fibronectin binding protein, FNZ.			253	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----287
XX	Fibronectin binding protein; SFS; vaccine; horse; strangles; therapy; equine upper respiratory tract disease; S. equi infection; FNZ.			254	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----288
KW				255	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----289
KW				256	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----290
OS				257	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----291
S				258	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----292
Streptococcus				259	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----293
equi				260	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----294
W020037496-A1.				261	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----295
PN				262	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----296
XX				263	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----297
XX				264	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----298
XX				265	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----299
XX				266	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----300
XX				267	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----301
XX				268	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----302
XX				269	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----303
XX				270	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----304
XX				271	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----305
XX				272	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----306
XX				273	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----307
XX				274	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----308
XX				275	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----309
XX				276	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----310
XX				277	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----311
XX				278	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----312
XX				279	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----313
XX				280	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----314
XX				281	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----315
XX				282	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----316
XX				283	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----317
XX				284	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----318
XX				285	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----319
XX				286	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----320
XX				287	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----321
XX				288	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----322
XX				289	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----323
XX				290	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----324
XX				291	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----325
XX				292	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----326
XX				293	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----327
XX				294	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----328
XX				295	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----329
XX				296	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----330
XX				297	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----331
XX				298	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----332
XX				299	-----MGRALKQLQPLNATKMRKQVPDF-----QLSIFESDK-----333

XX  
 XX  
 PI Guss B, Lindmark H, Jacobsson K, Frykberg L;  
 XX  
 XX WPI: 2000-442641/38.  
 DR N-PSDB; A30874.  
 PT New protein useful for preparation of vaccines for treatment of  
 PT strangles caused by *Streptococcus equi* infection, is able to bind to  
 PT mammalian fibronectin -  
 XX  
 PS Disclosure: Page 17a-17b; 34pp; English.  
 XX  
 CC This sequence represents the *Streptococcus equi* fibronectin binding  
 protein, FNZ. The FNZ sequence was used to isolate the *S. equi*  
 CC fibronectin binding protein of the invention, designated SFS. SFS binds  
 CC specifically to mammalian fibronectin or its analogues or fragments. The  
 CC protein, its analogues or fragments may be used for the preparation of a  
 CC vaccine that protects horses against strangles (a world-wide distributed  
 CC and serious disease of the equine upper respiratory tract) caused by  
 CC *S. equi* infection. The antibody and/or antiserum may also be used for the  
 CC prophylactic or therapeutic treatment of *S. equi* infection in mammal,  
 CC especially horses. The use of vaccines containing the fibronectin binding  
 CC protein provides a more effective protection against *S. equi* infections,  
 CC with fewer side effects.  
 XX  
 SQ Sequence 597 AA:

Query Match 4.6%; Score 180; DB 21; Length 597;  
 Best local Similarity 20.8%; Pred. No. 5; e-05;  
 Matches 149; Conservative 102; Mismatches 265; Indels 202; Gaps 34;

QY 68 SEIRWYGYESYVR-GHPYKQFRRVAHDURVNLEGRSVQVICKENLKKRAFPGLGDSVSKW 126  
 Db 32 aedlyygndgrtgqsypf--lyvskpnakreklekdeyvyeftnklywpdqwestysnf 89  
 QY 127 -----YKKHDGISTKREDYAMSPTGTDENQKLRAVMYNGHPQANGIMBG- 173  
 Db 90 ndirspryndlpryekkqydgikqkqspdykdkisalasavlslngqyptkksqistsy 149  
 QY 174 -LPLNLAIRTVQRAWYVYSDNAPISNPDESPKRESESNLVSLQSOLSLMRQALRQLDIPNL 232  
 Db 150 hLndssrkvtqjaiwyfsl-----sltkeylkatggnl-----ndmekkaldfiskge 200  
 QY 233 ATKMPKQVPPDQFLSIFEDKGDKYKNGQYQNLSSGIVLPTRPPTSGDPPMPNPQRTS 292  
 Db 201 dskl-kseqnyslidyyqsgghdmkyqnilstlipkeplp----- 245  
 QY 293 VLIRKYATGDSKLEGATLQTLGDDNNMSFQARVFSNSNDIGERIELSDQTYTLENSPA 352  
 Db 246 -----q1ggfs-----ghngnlgsgleggssgsgtne--dgkgl--1gfhg 284  
 QY 353 GYSIAE---PTh-FKVERAKVYTIDCKQKIQINPNKEIYEPYSVEAYNDFEERSVLTU 407  
 Db 285 g1sgssegkrkdp1pgkgegapd-----pkpndp1--agliegn-----spiveqn 330  
 QY 408 YARKFYAYRKNGQSSVVCNFADLKSPPDSEGGKTMPPDFITGEVKYTHING-----R 461  
 Db 331 y9s--tegyhgsgsile--etedtnppgqigggsgvne--thdetrphmgigqlag 383  
 QY 462 DLFKYTVKR-----DTBDPTFLKHKKVIEKGREKGKAIEVSGLTETQRLRAAQ 512  
 Db 384 esgettpqpgqgqgqpviettdt-----qkgmssqgqgtiesenttkpe 429  
 QY 513 LATYYFTDSAELDKKLKDHYHSGGMDNSTLAVAKKILVEYAQDSDNPQPLDQDFIPNN 572  
 Db 430 vmlggqgttectedtqk--gmssqggtie-----sdtkpkv----- 467  
 QY 573 KYOLSLGIGTQWHPEDLUDTIRMEDKKEVKIVPTVHNLTRKTVTGLAGDRKDFEIELKNN 632  
 Db 468 -----m1ggq-----qgildsen--tqsgmssqgqdt-----viedtk 500  
 QY 633 KQELLSQIVKTDKTNLEFDGKATINLKHGESITLQGL--PEGYSYLVKETDSEGIVKVK 690

Query Match 4.5%; Score 178; DB 20; Length 898;  
 Best local Similarity 18.6%; Pred. No. 0.00015;  
 Matches 171; Conservative 118; Mismatches 305; Indels 324; Gaps 42;

RESULT 3  
 W89413 standard; Protein: 898 AA.  
 XX  
 ID W89413  
 XX  
 AC W89413;  
 XX  
 DT 21-JUN-1999 (first entry)  
 XX  
 DE Moraxella catarhalis lactoferrin binding protein 2 (Lbp2).  
 XX  
 KW Lactoferrin receptor; lactoferrin binding protein; Lbp2;  
 KW lbpB gene; infection; otitis media; sinusitis; conjunctivitis;  
 KW pneumonia; bronchitis; tracheitis; emphysema; diagnosis; therapy;  
 KW vaccine; *Branhamella catarhalis*.  
 XX  
 OS Moraxella catarhalis.  
 XX  
 FH  
 FT Key Location/Qualifiers  
 FT Misc-difference 632  
 FT /note= "conserved epitope"  
 FT Region /note= "encoded by AAR"  
 FT /note= "conserved epitope"  
 XX  
 PN W09855606-A2.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 02-JUN-1998; 9880-CA00544.  
 XX  
 PR 08-MAY-1998; 98US-0074658.  
 PR 03-JUN-1997; 97US-0867941.  
 XX  
 PA (CONN) CONNAUGHT LAB LTD.  
 XX  
 PI Du R, Klein MH, Loosmore SM, Wang Q, Yang Y;  
 XX  
 DR WPI: 1999-070266/06.  
 DR N-PSDB; V82019.  
 XX  
 PT Lactoferrin receptor genes from *Moraxella*, especially *M. catarhalis*  
 PT - useful to diagnose *Moraxella* infection e.g. to detect otitis media  
 PT due to *M. catarhalis* infection and to immunise against such  
 PT infections.  
 XX  
 PS Claim 8; 202pp; English.  
 XX  
 CC This protein comprises lactoferrin binding protein 2 (Lbp2) of  
 CC *Moraxella catarhalis* (*Branhamella catarhalis*) 4223. It is  
 CC encoded by the lbpB gene of the lactoferrin receptor (lfr) locus  
 CC (see V72019) identified in the *M. catarhalis* 4223 genome.  
 CC Immunogenic compositions, including vaccines, based upon expressed  
 CC recombinant lbp1 and/or lbp2 and/or ORF3 proteins (see W8941-21),  
 CC portions of these, or their analogues, can be prepared for  
 CC prevention of diseases caused by *Moraxella*. *M. catarhalis* is a  
 CC causative agent of otitis media and has been associated with  
 CC sinusitis, conjunctivitis and inflammatory diseases of the lower  
 CC respiratory tract, such as pneumonia, chronic bronchitis,  
 CC tracheitis and emphysema.  
 XX  
 SQ Sequence 898 AA:

QY	4	TRPENKLUINTNTOVRLSKNSKRFTVTLVGFELMIFALVTSVMGAKTVFGVLESTPNATN	63	DE	Enterococcus faecalis antigenic polypeptide fragment EF104.
ID	1			XX	
QY	79	tdcpngangnqtlq-----aqtaaaagffm-----gkira	115	KW	Enterococcus faecalis; infection; vaccine; immune response; diagnosis; detection; attenuation; antigenic.
AC	2	tsk-----		KW	
XX	3	erhr-fdpkknktivqygnltpskuntyinhqadnknknknkpvdpv	98	XX	Enterococcus faecalis.
DT	4	pdysndivqwgklygida	116	OS	
QY	99	pdg19gtgknlrqptandikp	175	XX	
Db	100	lyfpkpfkpalnsdnihds	175	PN	W09850554-A2.
QY	148	GDELNQK-----LRAMVNGHQNANGIMEGLEPIN-----	178	XX	
Db	176	-----gssltqknaatpdndkdrripkpmplifng-----	178	PD	12-NOV-1998.
Db	176	-----erassqgkfnqytnwlysdvkrp	292	XX	
QY	179	ATRVQENWVYSDNAPISNPDESFKEKRESESNLVTSOSL-----	219	PF	04-MAY-1998; 98WO-US08959.
Db	293	alasaddrvgvynasgkn-----egdvvsaahylnfqykhptaqyvdfatn	343	XX	
QY	220	-MRQALKLKDLPNLATKPKQVDPDE-----QLSI	343	XX	
Db	235	SEDEK--GDNKNGQONLGG	269	PR	14-NOV-1997; 97US-0066009.
Db	344	gssltqknaatpdndkdrripkpmplifng-----	292	PR	06-MAY-1997; 97US-0044031.
QY	179	-----sitzklysydnpnqgtacgkysqfdttkkvnuetdvyqidak	403	PR	16-MAY-1997; 97US-0046655.
QY	270	L-----VPTKPTGPDPMPNPQPTSVLIRKAYGDYKSKILEGATLQ	321	XX	
Db	404	QTSVLTTELNPSAGYSIAEPITFKEVAGKVTIDG-----	375	XX	
QY	322	FQARVFSSND-----IGERIELSDGTYTTLTELNPSAGYSIAEPITFKEVAGKVTIDG	375	PA	(HUMA-) HUMAN GENOME SCI INC.
Db	443	--agkfisndnasyvvrfgkrkdkpkvaktvysaqe--kptstvrdnetigrins	498	XX	
QY	376	KOJENPNEKEIVE---PVSEAYNDF-----ERFSVJMTN-----YAKFVYAK	415	PT	
Db	499	-----kkindavnekeidngdptsderydefpwgekkaeftkkvssstqavpayrqhakfyf--	556	PT	
QY	416	NKNGSSQVYCEVENDLKSPPDSBGGKMMTPDFTGEV-----	453	DR	WPI: 1999-070095/06.
Db	557	--ngnyyvalsssvdklapadavkandskiekypnatinkdnqytaivlqea	614	DR	N-PSDB; X20201.
QY	454	--KYHIA-GRDLF-----KIVKPRDTPDFFLHKKVI-----	486	XX	
Db	615	1raksyqhisgetlyndanqntptrsyzfwqggradsttlpkqkftqynglwqyliqkk	674	XX	
QY	487	EKGYREKGQAIYEVSG-----LTENQLRANTQALIYYFT-----DSAELDKDKUDYIGF	535	CC	
Db	675	-----dkqgynneetikkghqdyilted-----fpeddddtassdssqddahq	722	CC	
QY	536	GMDNDSLAVAKTILVEYQDSNPOLTDIFPNNKQYQSLGTOBWEVDLIDIRMD	595	CC	
Db	723	536-----asddsqqddadgddssdl-----gddaddaaagkvvhagn-----irpef	767	CC	
QY	596	KKEVIPV-----THMLT-----RKTIVGLADKDRKDHFEEELKKNQEL	637	CC	
Db	768	637-----enkyuipineptektfalgknkpfavdfdtntsltgkinderqdivfai-----knkgidg	825	CC	
QY	638	SQVTKTKTINLKEFGKATINLKHEGSELTQGLPEGYSYLVKENTDSEGKVVKVNSQEVA	696	CC	
Db	826	696-----gftakadavpnyreevg-----nnqgg-----gfyinikldvkqggffgtngelag	871	CC	
QY	697	-----NATVSKTG	704	CC	
Db	872	872 q1qydkdgindtaekag	889	CC	
RESULT	4	Sequence	1416 AA;	XX	
Y00211		Query Match	4.1%; Score 161; DB 20; Length 1416;		
ID		Best Local Similarity	21.1%; Pred. No. 0.0059;		
Y00211		Matches	159; Conservative 104; Mismatches 326; Indels 166; Gaps 40;		
XX		Matches	159; Conservative 104; Mismatches 326; Indels 166; Gaps 40;		
AC		Matches	159; Conservative 104; Mismatches 326; Indels 166; Gaps 40;		
XX		Matches	159; Conservative 104; Mismatches 326; Indels 166; Gaps 40;		
DT		Matches	159; Conservative 104; Mismatches 326; Indels 166; Gaps 40;		
QY	39	ALVTSVYAKVNVFGIVES-----STPNAINPSSSERFWYGEYESYVKGHPPYKQFRVADLR	95	QY	39 ALVTSVYAKVNVFGIVES-----STPNAINPSSSERFWYGEYESYVKGHPPYKQFRVADLR
Db	484	-----gkira-----	95	Db	484 -----gkira-----
QY	96	--VNELEGSRSYQVYCFNLKKRAFP-----LGDDSSVWKWVKKHDGISMIFEDYAMSRITGD	149	QY	96 --VNELEGSRSYQVYCFNLKKRAFP-----LGDDSSVWKWVKKHDGISMIFEDYAMSRITGD
Db	532	532 ttvsvngskeskpiqkleikvkhpnjyislratkeifyyk-----gt-----dytvptsdgs	584	Db	532 ttvsvngskeskpiqkleikvkhpnjyislratkeifyyk-----gt-----dytvptsdgs
QY	150	150 ELNQKLRAVMYNGHQNANGIMEGE-----PLNIRVTOBAWVYSDNAPISNPDESFK	204	QY	150 ELNQKLRAVMYNGHQNANGIMEGE-----PLNIRVTOBAWVYSDNAPISNPDESFK
Db	585	585 vikfttpitheiqlpifgfnvpdslpdkcipdipitmaeglptvdtvtt-----nsk	641	Db	585 vikfttpitheiqlpifgfnvpdslpdkcipdipitmaeglptvdtvtt-----nsk
QY	205	205 RESENVLVTSQSLSTMRQAKLQKLIPLNATKMPKQVPPDDFOLSLIESEDKGDKYKRYG	313	QY	205 RESENVLVTSQSLSTMRQAKLQKLIPLNATKMPKQVPPDDFOLSLIESEDKGDKYKRYG
Db	642	642 rgsrtlqsknqfvnarnsdfsdsrvrtkipada-----dvlfdiyavsn-----dqvsiy	697	Db	642 rgsrtlqsknqfvnarnsdfsdsrvrtkipada-----dvlfdiyavsn-----dqvsiy
QY	265	265 LLSGGI1VPTKPTGPDPMP-----PNQPTISVLI-----RKYAICDDYSL-----LEGATLQ	313	QY	265 LLSGGI1VPTKPTGPDPMP-----PNQPTISVLI-----RKYAICDDYSL-----LEGATLQ
Db	698	698 ywdqgqyfdkpmptpspgyptifentusytfdgktpkryi-----eyknangdwidp	756	Db	698 ywdqgqyfdkpmptpspgyptifentusytfdgktpkryi-----eyknangdwidp
QY	314	314 LTG-----DNVNSFQARVFTSSNDIGERIELSDGTYTTLTELNPSAGYSIAEPITFKEVAG	367	QY	314 LTG-----DNVNSFQARVFTSSNDIGERIELSDGTYTTLTELNPSAGYSIAEPITFKEVAG
Db	757	757 itgrakapeqsnmneqasavsvqn-----ealdilsat-----qanptiknvkt	801	Db	757 itgrakapeqsnmneqasavsvqn-----ealdilsat-----qanptiknvkt



XX	DE	Photorhabdus luminescens insect toxin TcdAII.
KW	Insecticide; insect; toxin; pest control; biological control;	3-9%; Score 154; DB 18; Length 1849;
KW	Photorhabdus luminescens; TcdA; Southern corn rootworm;	Query Match 157 AVMNIGHFNPQANGMEGEPLNARVTOE-AVWYSD-----NAPISNPDESEKRESE 209
KW	Colorado potato beetle; Western corn rootworm; meal worm;	Best Local Similarity 18 3%; Fred. No. 03; Mismatches 148; Matches 148; Conservative 120; Indels 254; Gaps 37;
KW	boil weevil; turf grub; Coleoptera; beet armyworm; black cutworm;	Matches 148; Conservative 120; Mismatches 287; Indels 254; Gaps 37;
KW	cabbage looper; coding moth; corn earworm; European corn borer;	
KW	tobacco hornworm; tobacco budworm; Lepidoptera; Hymenoptera;	
KW	Diptera; Dictyoptera; Acarina; Homoptera.	
XX	OS	Photorhabdus luminescens strain W-14 (ATCC 55397).
XX	FH	Key location/Qualifiers
XX	FT	Protein 1:1849
XX	FT	Peptide /label= TcdAII
XX	FT	1..12
XX	FT	/note= "S2 N-terminus (Claim 30)"
XX	FT	196..211
XX	FT	Peptide /note= "trypptic peptide (Claim 30)"
XX	FT	466..475
XX	FT	/note= "trypptic peptide (Claim 30)"
XX	FT	993..1004
XX	FT	/note= "isolated N-terminal peptide (Claim 30)"
XX	FT	1297..1312
XX	FT	Peptide /note= "trypptic peptide (Claim 30)"
XX	FT	1390..1409
XX	FT	/note= "trypptic peptide (Claim 30)"
XX	FT	1532..1554
XX	FT	Peptide /note= "claimed peptide (Claim 30)"
XX	PN	W09717432-A1.
XX	PD	15-MAY-1997.
XX	PF	06-NOV-1996; 96WO-US18003.
XX	PR	28-AUG-1996; 96US-0705484.
XX	PR	06-NOV-1995; 95US-0007255.
XX	PR	28-FEB-1996; 96US-0608423.
XX	PA	(WISC ) WISCONSIN ALUMNI RES FOUND.
XX	PI	Blackburn MB, Bowen DJ, Ciche TA, Ensign JC, Fatig R; French-Constant RH, Guo L, Hey TD, Merlo DJ, Orr GL; Petell J, Roberts JL, Rocheleau TA, Schoonover S; Strickland JR; DR
XX	PR	WPI; 1997-281022/25.
XX	DR	N-PSDB; T68844.
XX	PT	Photorhabdus sp. insecticidal protein toxins and DNA encoding them - can be genetically engineered into insect larvae food and plants for insect control
XX	PS	Claim 34; Page 201-208; 276PP; English.
CC	This polypeptide comprises the 209-2 kDa TcdAII insecticidal toxin protein of Photorhabdus luminescens W-14. Its sequence was deduced from a genomic DNA clone (T68844) and includes N-terminal and tryptic peptide sequences obtained from the isolated protein. TcdAII is a proteolytic cleavage product of TcdA (see W17899).	3-9%; Score 154; DB 18; Length 1849; Query Match 157 AVMNIGHFNPQANGMEGEPLNARVTOE-AVWYSD-----NAPISNPDESEKRESE 209
CC	Claimed toxins of P. luminescens (see W17871, W17881-89, W17899-900, W18301-06) can be produced by recombinant DNA methods and applied to, or genetically engineered into, insect larvae food and plants for insect control. The toxins are particularly effective against Southern corn rootworm, Colorado potato beetle, Western corn rootworm, meal worm, boil weevil and turf grub (Coleoptera), beet armyworm, black cutworm, cabbage looper, coding moth, corn earworm, European corn borer, tobacco hornworm and tobacco budworm (Lepidoptera), and are also active against insects of the orders Hymenoptera, Diptera, Dictyoptera, Acarina and Homoptera. (All claimed).	Best Local Similarity 18 3%; Fred. No. 03; Mismatches 148; Matches 148; Conservative 120; Indels 254; Gaps 37; Matches 148; Conservative 120; Mismatches 287; Indels 254; Gaps 37;
CC	RESULT . 7	
CC	W56573	W56573 standard; Protein: 1849 AA.
CC	AC	W56573;
CC	XX	07-AUG-1998 (first entry)
CC	DE	Toxin TcdAII, encoded by the tcdA gene from genomic region tcd

XX  
 KW Photorhabdus luminescens W-14; nematode; symbiotic;  
 KW Heterorhabditis; tca; tcb; tcc; tcd; insecticidal activity; toxin;  
 KW Lepidoptera; Coleoptera; Hymenoptera; Diptera; Dictyoptera; Acarina;  
 KW Homoptera; Southern, Western corn rootworm; Colorado potato beetle;  
 KW mealworm; boll weevil; turf grub; beetle armyworm; black cutworm;  
 KW cabbage looper; coding moth; corn earworm; European corn borer;  
 KW Tobacco hornworm; budworm.

XX  
 OS Photorhabdus luminescens.

XX  
 PN W09808932-A1.

XX  
 PD 05-MAR-1998.

XX  
 PR 05-MAY-1997; 97WO-US07657.

XX  
 PR 06-NOV-1995; 96WO-US1803.

PR 06-AUG-1995; 96US-0705484.

PR 06-NOV-1995; 96US-0743699.

XX  
 PA (DOWC ) DOWELANCO.

PA (WISC ) WISCONSIN ALUMNI RES FOUND.

XX  
 PR Blackburn MB, Bowen DJ, Ciche TA, Ensign JC, Fatiq R;  
 PI Ffrench-Constant RH, Guo L, Hey TD, Merlo DJ, Orr GL;  
 PI Petell J, Roberts JH, Rochelleau TA, Schoonover S;  
 PI Strickland JA, Sukhapinda K;

XX  
 DR WPI; 1998-179427/16.

DR N-PSDB; V2930.

XX  
 PT Isolated toxins from Photorhabdus luminescens strains - useful for  
 PT control of insect pests.

XX  
 PS Claim 34; Pages 238-243; 321pp; English.

XX  
 CC The present sequence represents a protein named TcdA1 of the bacterium  
 CC Photorhabdus luminescens (W-14). This is a symbiotic bacterium of the  
 CC nematodes of the Heterorhabditis genus. The bacterium has at least 4  
 CC distinct genomic regions, tca, tcb, tcc, and tcd. Peptide products are  
 CC produced from these regions that are associated with insecticidal  
 CC activity. The native toxins are secreted proteins. The proteins are  
 CC toxic to insects upon exposure and especially when ingested. The  
 CC nucleic acid sequence can be used to produce transgenic plants',  
 CC baculoviruses or microbial hosts for toxin production. They can be used  
 CC to control insects pests from the Lepidoptera, Coleoptera, Hymenoptera,  
 CC Diptera, Dicynoptera, Acarina or Homoptera orders, especially the  
 CC Southern or Western corn rootworm, Colorado potato beetle, mealworm,  
 CC boll weevil, turf grub, beetle armyworm, black cutworm, cabbage looper,  
 CC cooling moth, corn earworm, European corn borer or tobacco hornworm  
 CC or budworm.

XX  
 SQ Sequence 1849 AA;

RESULT 8

W17899 ID W17899 standard; Protein; 2516 AA.

XX AC W17899;

XX DT 29-JAN-1998 (first entry)

XX DE Photorhabdus luminescens insect toxin TcdA.

XX Insecticide; insect; toxin; pest control; biological control;

KW Photorhabdus luminescens; TcdA; Southern corn rootworm;  
 KW Colorado potato beetle; Western corn rootworm; meal worm;  
 KW boll weevil; turf grub; Coleoptera; beet armyworm; black cutworm;  
 KW cabbage looper; coding moth; corn earworm; European corn borer;  
 KW tobacco hornworm; tobacco budworm; Lepidoptera; Hymenoptera;  
 KW Diptera; Dictyoptera; Acarina; Homoptera.

OS Photorhabdus luminescens strain W-14 (ATCC 55397).

XX FH Key Location/Qualifiers

FT Protein 1..2516  
 FT /label TcdA

FT Protein 89..1937

FT Peptide /label TcdA1  
 89..1100  
 /note "S2 N-terminus (Claim 30)"

FT Peptide 284..299  
 /note "tryptic peptide (Claim 30)"

Db 974 qsvsqqlnadtvedafmsyltsfseqvanlvkisaydninddgltiyfiglsetdagey 1033

Oy 335 ----RIEISDGTYVLT----EINSPAG--YSAEPTFFKVKVYTI-IDGKQIE 379

Db 1034 ywrsvhskfhgkfaanawsewhkicdcpinpykstirpivk--srylylwiegkeit 1090

Oy 380 NPNKEVVEPVSYEAVNDFE-----EFSVLTQN----YAKF 411

Db 1091 kqtgqskdqyqettdyryeklahirydgwtntptifdvnnkkisekleknrapglyca 1150

Oy 412 YVAKN-----KNGSSQVVICFNADLKSPPDSEDGKTMW----- 446

Db 1151 yqgedtlvmyfnyqqtldsykasmqglif-admas-----kamtpeqsvyrdn 1201

Oy 447 -----DFTGEVKVTHIACRDLFKYTVKRDRDTP 475

Db 1202 syqqfqttnvrvnryaedyelppsvssskdygwgdyylsmvnyngdpttinykaassd1 1261

Db 1322 ysg---ntsngnqrll--fhrdtyp--skveawipgakrsitnqnaigdyatds1 1373

Oy 583 -HPELDVDIRMEDREKVI---PVTHNLTL--RKTVYGLAGDRTKRHF----- 626

Db 1374 nkpdikqyifmtdksgtataovsgpveintaispavkqviikaggkeqftadkvsip 1433

Oy 627 -----IELKNNKQELLSQTVKDKTNIEF-KQK-----ATINKHQ 662

Db 1434 spsfdeomyqfnaleidsglnfinnsasidntftafadegrklygesfsipvtkvstd 1493

Oy 663 ESTIIGLSPCEYSLVKEITSEGVKVKNS--QEVANNTSKGISEDETAFENKE 718

Db 1494 naltlhnnegaqym---qwsytrntlfarqvarat--tgidtilsmetqniqe 1546

Oy 719 PVVPTGVQDKINGYIALIVTAGISIGWG 747

Db 1547 P-----qlgkgfifatfivppypnlisthg 158





DR WPI; 1999-357844/30.  
 DR N-PSDB; X77593.  
 XX PT Staphylococcus aureus fibrinogen-binding proteins for treating  
 PT septicemia, osteomyelitis, mastitis or endocarditis  
 XX PS Claim 8; Fig 8; 143pp; English.  
 CC This invention describes novel Staphylococcus aureus fibrinogen-binding proteins that bind both the alpha and beta fibrinogen chains. The proteins and their encoding nucleic acids are ClfB, SdrC, SdrB and SdrE. Staphylococcus aureus is thought to utilize fibrinogen to adhere to medical devices, binding proteins that bind both the alpha and beta fibrinogen chains (ClfB, SdrC, SdrB and SdrE) can therefore be used as competitive inhibitors to block this binding. Antibodies against ClfB, SdrC, SdrB and SdrE inhibit ClfB, SdrC, SdrB and SdrE mediated binding. The proteins of the invention can be used in a pharmaceutical composition for the treatment of Staphylococcus aureus infection e.g. septicemia, osteomyelitis, mastitis or endocarditis or to inhibit the binding of S. aureus to the extracellular matrix. The proteins or their fragments may be used to coat a medical device to reduce the S. aureus infection of an indwelling medical device, especially where the medical device is selected from the group consisting of vascular grafts, vascular stents, intravenous catheters, artificial heart valves, and cardiac assist devices. ClfB, SdrC, SdrB, SdrE, or an active fragment, subdomain or encoding gene may be used as a vaccine. The DS (aspartate serine) repeat region or a gene encoding it may be used as an identifying probe for the identification of genes and encoding proteins from Staphylococcus aureus (other than ClfA). S. hemolyticus, S. lugdenensis, and S. schleriferi. The proteins of the invention have antibacterial activity.

CC XX Sequence 1315 AA;

Query Match 3.8%; Score 149; DB 20; Length 1315;  
 Best Local Similarity 20.2%; Pred. No. 0.041; Gaps 45;

Matches 203; Conservative 93; Mismatches 336; Indels 372; Gaps 45;

QY 8 NKLNLNTQTVQLSNS---KRFTVTILVGVLFIMIAVTSWAGAKTVFGLVESSTR---- 59

Db 208 nsnnennadilpkstapkrlntr----mriaavqpssteakvnditstnlttvda 262

QY 60 ---WAINP---DSSSERWYRGYESVYRGRHPYKQKORVADLRLVNLLEGSRSYQVFCNLKKA 114

Db 263 dknnkivpadylsksqitvdvdkvksqdf----tikytsdvqvygipedi 311

QY 115 FPLGS---DSSVKKWKKHDG---ISKFEDYAMSPRITGDELNQKLRAMVNGH--- 163

Db 312 knigdikdpnqgetlatakhdtaanlitytfddy----dfnsvqmginyjsynda 364

QY 164 ---PQANGTMEGIEPLPNAIRVTOBAWVYSDNAPISNIDESFKRESESNL---- 211

Db 365 dtipvsknadvfnvtingttkttaniqpdyvvnenknsigasftetvhvgnkenpgyy 424

QY 212 -----VSTQSLSLMRAALK---QIDPMLATKAPKQVDFDQFQFEESEDKGKYNKGY 262

Db 425 kqtiqlyvpsensltnaklkvqayhssyppnqinqkdvrd---ikiyq-vpkgytlnkgy 480

QY 263 QNLISGGLUPTKPPPIPQDPMPQNPQTSVSLIRKKAIDYSK---- 305

Db 481 d-----vntkeit----dvnqyiqkitygdnnasavidfgnadsavymvn 522

QY 306 -----LIEGATQLTGD---- 319

Db 523 tkfqytntseptlvqmatlsstgnksvstgnalqftnqsgqgqeqvkyignywedtnk 582

QY 320 NSFO-----ARVSSN---DIGERIEUDGDTYMTL-----NSPAGIS 355

Db 583 ngvqelgekqgvgnvrtvfdantntkvgeavtkedgqsyliplpnqdyrvefsplkgye 642

QY 356 IAE----- 358

Db 643 vtpskqgnneeldsngllssvivtngkgnlsadlgiykpkylnqdyvwdtnkngiqdqe 702

QY 359 -----PITFKVEAGKVY---TIDG---QIENPKEI----VEPYSVEAKNDF 397

Db 703 kgisqvtvltkdenqnvktvtdgkqftldngqkvettpeyptvtsgsd 762

QY 398 EEEFS-VLTTONY-----AKFYAKRNKNQSSQVYCFNADLKSPPDSE---GGKT 443

Db 763 ekdsnglttgvngadmtldsfyktptkynignywedtnkdgq -dslekqisqvt 820

QY 444 MTPPTITGKVYTHIAGRO-LEKTYVKRPTDPTFLKHKKVIEKGYREKSGAEY--- 499

Db 860 sgyptqyqsgtadsgnqgtstqgvkdkndtdsgfkykpytnlgqywedtnkngqvg 919

Db 821 vtlnnengevlqtktdkdgkyif-----qlengthykvetept 859

QY 537 DMNDSTLAVA-----KILVEAQDSNPP-QLTDIDFFINNNKQYQSLICQWHRD 586

Db 920 dkdekgisqvtvltkdenqnvktvtdgkqftd-----nngtyk----- 963

QY 587 LDIRFMEKKEVIP---VHNLTURK----TYNGL---AGDRTRKDFREIELNKNOEL 636

Db 964 ---vefetpsqyptsvsngnakekdnsqnglttpeyvkdadmtldsf---ytkpksl 1016

QY 637 -----LSQTVKDITKNEFLFKOKATINLKHESLTLOGLPGGYSYLVKEDSEGYKV 689

Db 1017 qdywydshkdgkdgstergikdykvtnlnegevigtkttdengkycfanladsqkyvi 1076

QY 690 VNSQEVANATVSKGITSBETLAFFENKEVPPVPGDOKI-NSY 732

Db 1077 f--ekpagitqtgtnteedkddaggevdtvtdhadtldngy 1118

RESULT 11

Y00238 ID Y00238

XX standard; Protein: 2032 AA.

XX AC Y00238;

XX DT 20-APR-1999 (first entry)

XX DE Enterococcus faecalis protein EF123.

XX KW Enterococcus faecalis; infection; vaccine; immune response; diagnosis; detection; attenuation; antigenic.

XX OS Enterococcus faecalis.

XX PN WO9805054-A2.

XX PD 12-NOV-1998.

XX PF 04-MAY-1998; 98WO-US00959.

XX PR 14-NOV-1997; 97US-0066009.

PR 05-MAY-1997; 97US-0044031.

PR 16-MAY-1997; 97US-0046655.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Bailey C, Choi GH, Hromockyj A, Kunsch CA;

XX DR WPI; 1999-070095/06.

DR N-PSDB; X20228.

XX PT New isolated Enterococcus faecalis polynucleotides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus infection

XX PS Claim 9; Page 224-225; 301pp; English.

XX CC The present sequence represents a protein isolated from

Sequence	3032 AA;	Query Match	3.8%	Score	149;	DB	20;	Length	2032;
CC	Enterococcus faecalis	Best Local Similarity	19.0%	Pred. No.	0.083;	Matches	178;	Conservative	117;
CC	and antigenic polypeptides isolated from E. faecalis.	Mismatches	330;	Indels	310;	Gaps	178;	Mismatches	330;
CC	The proteins can be used in vaccines for preventing or attenuating an infection caused	by a member of the Enterococcus genus in an animal.	They can also be	used for detecting Enterococcus antibodies in a sample.	The nucleotide	sequences can be used for detecting Enterococcus nucleic acids.	products from the present invention can also be used for screening	compounds to identify agonists and antagonists of E. faecalis protein	activity.
CC	CC	CC	CC	CC	CC	CC	CC	CC	CC
XX	SQ	Qy	19	LSKNSKRRTVTLYGVFLMFALVTSWV-----GATVFG-----LVESTTPNAT	62	Db	1098	IKKTTAEDTTLAGAHFQIWDQAKTQVIREGTVQATGVITFGGIPQQQVILVETKAP--	1154
Qy	63	NPDSSEVERWYGVESYVHGPYKQFRAHDLRVNLEGRSRYQYVCFNLKAFPLGSDS	122	Db	1155	-----egytvsdelakgrvittideetsaegqap-tilkndvkvflekmek	1200	Qy	123
Qy	123	VKKW---YKKHDISTKF--EDYAMSRITGDELNQKLRAVYNGHQNANGIME-G	173	Db	1201	gkvlvnafklehvttptfhwveplapprt-----nangglevs	1242	Qy	174
Qy	174	LFP-LNIRRTOAWKY'SDNAP-----ISNPDESKRESESN	210	Db	1243	lkpglyqftteleaptgyldtppkrfrvtqntsgqirdhvkmlyqgqsaelikkdqagn	1302	Qy	211
Qy	211	IVSTRSQSLM--ROALQK--LIDPNLAKTAKMPKQVPPDDLSITESEDKDQKYNQGYNL	265	Db	1303	plagaefsvldttqgaviehvldangkvvtvdlapgkqf---vetkap-----1349	1303	Qy	266
Qy	266	LGGGLVPKPPGDPMPMPNQQT-----TSYLVIRKVAIGDYSKLEGATLQ	313	Db	1350	-agylintepsaftiaasdrgkpatvianfanvnyqgtaklikdvng--hlsqatfk	1405	Qy	314
Qy	314	LTGDNVNSFQARVFSSNDIGERI--ELSGTYTLELNSPAGYST-AEPIFKV--EAG	367	Db	1406	368 K-----vldakgetiqtg1-ttnnqgeleahlgapkgkyrvetkaptgylnttpwfpfelaeknag	1464	Qy	411
Qy	411	-----VTTIDCOIENNKEVPEVSYEAYNDFREEFSYLTTONAK--	410	Db	1465	kpavvvasdndfsykgafqivkntsaddplagav---fely-dinkqsigatstgkdg	1519	Qy	498
Qy	498	-----FVYAKN-----NGSSQWYC-----FNADLKSPPDSEDDGKTMTPDF	448	Db	1520	kilfrdlapqyykeiakapklpdgadyiypelvkveirgdfkqdpel-----f	1569	Qy	449
Qy	449	TGEVKVTHIAGRLFLKVTKPROTDPTDFLKHKKVIRGYR-----EKGQAI--	497	Db	1570	q1g---atafnkgravfkidananplpgtifiklyr--lengkeferevtaekdslame	1625	Qy	577
Qy	577	-----LIGTQWHPEDLVDIRMEDKKEVIPVHNLTLKTVTGLADGRKDFHEIELK	630	Db	1686	541 STLAVAKILIVEAQDSNPQPLDUDFFPNNNNKQYOS-----	576	Qy	541
Qy	541	541 STLAVAKILIVEAQDSNPQPLDUDFFPNNNNKQYOS-----	576	Db	1790	631 NNIKQELLSQTV--KTDKTNLEFKDQGKATT-NLKHZGESLTLQGLPEGY-----SYLV	678	Qy	631
Qy	631	631 NNIKQELLSQTV--KTDKTNLEFKDQGKATT-NLKHZGESLTLQGLPEGY-----SYLV	678	Db	1746	1686 qtlagavfaivnadeqndqpgspfittflnragekvseittdtkgeiyakqglneghyvvet	1745	Qy	1746
Qy	1746	1746 kaptgyldttdlhp---fadvtaqiqkeapialgdlinyqta-----qitke	1789	Db	1790	netgealagavfkvideg-qttdqgtlmlsdkgkvialqngtyrfretqaptsyli	1848	Qy	1790

QY 123 VKKW---YKKHDGISTKF---EDYAMSRITGDELNLQRKRAVMYNGHPONANGIME-G 173  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1201 gkklvnrarflehvaptptphtwewplapdt-----naqglevs 1242  
 XX  
 PR 04-MAY-1998; 98W0-US08959.  
 PR 14-NOV-1997; 97US-0066009.  
 PR 06-MAY-1997; 97US-0044031.  
 PR 16-MAY-1997; 97US-0046655.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Bailey C, Choi GH, Hromockyj A, Kunisch CA;  
 XX  
 DR WPI; 1999-070095/06.  
 DR N-PSDB; X20232.  
 XX  
 PT New isolated Enterococcus faecalis polynucleotides - used to develop  
 PT for prevention or attenuation of Enterococcus infection  
 XX  
 PS Claim 9; Page 232; 301PP; English.  
 CC The present sequence represents a protein isolated from  
 CC Enterococcus faecalis. The present invention describes genes, proteins  
 CC and antigenic polypeptides isolated from E. faecalis. The proteins can  
 CC be used in vaccines for preventing or attenuating an infection caused  
 CC by a member of the Enterococcus genus in an animal. They can also be  
 CC used for detecting Enterococcus antibodies in a sample. The nucleotide  
 CC sequences can be used for detecting Enterococcus nucleic acids.  
 CC Products from the present invention can also be used for screening  
 CC compounds to identify agonists and antagonists of E. faecalis protein  
 CC activity.  
 XX  
 SQ Sequence 2032 AA;

Qy 541 STLAVAKILIVEYAADSNPPQTDIFEPINPKYQS----- 576  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1686 qtlagavfainyadengnqspgspitflnragkeyseittdktgeiyakglneghyvvet 1745  
 Matches 178; Conservative 117; Mismatches 330; Indels 310; Gaps 44;  
 Qy 577 -----LIGQWHPPEDLVDLDIRMEDKEVKEPVTHNLRLTRKTVTGLADRKDFHEIELK 630  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1746 kaprgyliidtlhp---fdvtaqjgkeqpalgdlinyqta-----qtlke 1789  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 631 NNKQFLSLSQTY--KTDTNLEFKDGKATI-NLKIGESELTLQGLPBGY-----SYLV 678  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1790 netgealagavfkvidty-qtvqagqtnlmsdkqgkvianlqgtyrvtqaptysil 1848  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 679 KETSESEGYK----- 698  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1849 netpsasftiakdnqgkpatvvlkapfinyygaaklviqdkqkhnallagaefkvtdaetq 1908  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 699 TVSKKIGITSDETLAFENNEKEPVVPGVQDQKI-NGY 732  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1909 tvarslrsdqnglyqvnhlqpgkytfvetkapdg 1943  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 RESULT 13  
 ID Y00242 standard; Protein; 2032 AA.  
 XX  
 AC Y00242;  
 XX  
 DT 20-APR-1999. (first entry)  
 XX  
 DE Enterococcus faecalis protein EF125.  
 XX  
 DE Enterococcus faecalis protein EF125.  
 XX  
 KW Enterococcus faecalis; infection; vaccine; immune response; diagnosis;  
 KW detection; attenuation; antigenic.  
 XX  
 OS Enterococcus faecalis.  
 XX  
 PN W09850554-A2.

QY 123 VKKW---YKKHDGISTKF---EDYAMSRITGDELNLQRKRAVMYNGHPONANGIME-G 173  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 XX  
 PD 12-NOV-1998.  
 XX  
 PR 04-MAY-1998; 98W0-US08959.  
 XX  
 PR 14-NOV-1997; 97US-0066009.  
 PR 06-MAY-1997; 97US-0044031.  
 PR 16-MAY-1997; 97US-0046655.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Bailey C, Choi GH, Hromockyj A, Kunisch CA;  
 XX  
 DR WPI; 1999-070095/06.  
 DR N-PSDB; X20232.  
 XX  
 PT New isolated Enterococcus faecalis polynucleotides - used to develop  
 PT for prevention or attenuation of Enterococcus infection  
 XX  
 PS Claim 9; Page 232; 301PP; English.  
 CC The present sequence represents a protein isolated from  
 CC Enterococcus faecalis. The present invention describes genes, proteins  
 CC and antigenic polypeptides isolated from E. faecalis. The proteins can  
 CC be used in vaccines for preventing or attenuating an infection caused  
 CC by a member of the Enterococcus genus in an animal. They can also be  
 CC used for detecting Enterococcus antibodies in a sample. The nucleotide  
 CC sequences can be used for detecting Enterococcus nucleic acids.  
 CC Products from the present invention can also be used for screening  
 CC compounds to identify agonists and antagonists of E. faecalis protein  
 CC activity.  
 XX  
 SQ Sequence 2032 AA;

Qy 19 LSKNSKRIFTYLGVFLMFALVYSM-----GAKTVFG-----LVPSSTPNAL 62  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1098 lktkamdettilagahfqwdqaktqvirkvqtvatgvtffgqipqggylivvetkap-- 1154  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 63 NPDSSSEYRWYGYESYVRGHPYQFRVADLRLRNLEGRSRSYQYCFNKKAPLGSSS 122  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1155 -----egytvsdelagravitideetsaegaq-ptikndwnkvflekmdek 1200  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 123 VKKW---YKKHDGISTKF---EDYAMSRITGDELNLQRKRAVMYNGHPONANGIME-G 173  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1201 gkklvnrarflehvaptptphtwewplapdt-----naqglevs 1242  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 174 LEP-LNARVTOEAWWYSDNA----- 210  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1243 lkglyqfieaptgylidttptkrfrtvqntsgqirdhvkmlnyqgsaelkkdagn 1302  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 211 LVTSQSLSM---ROALKO---LIDPNLATKMPKQVPPDFQLSIFESEDKGDKYNGQNL 265  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1303 plagaefsvdttgavrehlvsdangkvvtlapgkqf---vetkap----- 1349  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 266 LSGGIVPTKPTPDPMPMPNQQT-----TSVLIRKYAIGDYSKLEGATQ 313  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1350 -agylintepsaftiadasdrgkpatvianfnvnyqgtralikkdng---hilsatq 1405  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 314 LTGDWVNSFOARVSSNDIGERI---ELSDCTYLTTELNSPAGSI-AEPITFKV--EAG 367  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1406 vldakgetiqtql-ttnqnggeivahlapgkqfrvethkaptgylnttpypfieaknag 1464  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 368 K-----VTTIDGKQIENPNKEVPEPYSEAYNFEESVLTTONYAK-- 410  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Db 1465 kpavvavsfvsvykgafqivktnsadqplagav---fely-dhnsqsligatsgkdg 1519  
 ||| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 Qy 411 -----FVYAKNK---NGSSQVYC----FNADLKSPPDSEDGKTMTPDF 448

Db 1520 kilfrdlapgttyykeikapklpgadyyiypelvkeirgdfkgdei ..... f 1569  
 QY 449 TTGEVYKTYHTLAGRDIFKTYVKPRDDPDTFLKHKKVIEKGYR-----EKQAI--- 497  
 Db 1570 qlg-afanfkgravfkkidananplgtfklyr-iengekiferevtaekslane 1625  
 QY 498 -----EYSGLTERQTLRATAOLAYYF---TDSAEELDKDKLKDYHG--FG---DMND 540  
 Db 1626 dlgaqsyeldatdgyivnqkpiyfvvkknsndkqplidefvnyqgevngkvneqg 1685  
 QY 541 STLAVALKILVEYAAOSNPOLTDDEFIFPNKKQG-..... 576  
 Db 1686 qtlagavfaiynaedeqnpgspafplnraagekseitdtgeiyakgnginehyvvet 1745  
 QY 577 -----LIGTQWHPEDLVDLDIRMEDKEVTPVTHNLRLRKVUTGLAGDRDKFHFIEELK 630  
 Db 1746 kaptjyldtlhp---fdtaqlgkeqpiagldinygta-----gltke 1789  
 QY 631 NNKQELISORTV-KRDKTNLEFKOCKATI-NLKQGESLTLQGLPEQY-----SYLV 678  
 Db 1790 netgealagavfkvidetg-qtvadqgtnlmsdkqgkviaknlapgttyrvfetqaptysl 1848  
 QY 679 KETDSGCK-----VKNSQEVAN----- 698  
 Db 1849 netgealagavfkvidetg-qtvadqgtnlmsdkqgkviaknlapgttyrvfetqaptysl 1908  
 QY 699 TVSKGQTGTSDETLAFENKEPVVPTGVDQKI-NGY 732  
 Db 1909 tvartsrdsnglyqvwhlqpgkyfvetkapdg 1943

**RESULT 14**  
 ID R22675 standard; Protein: 1185 AA.  
 AC R22675;  
 XX DT 04-DEC-1992 (first entry)  
 XX DE Collagen binding protein.  
 XX KW CBP; collagen binding protein; mastitis; arthritis.  
 XX OS *Staphylococcus aureus*.

PH Key Location/Qualifiers  
 FT Region 30..1185  
 FT Peptide /note= "claim 11; page 29-30"  
 FT Region 1..29  
 FT Region 30..1534  
 FT Region /label= A /note= "see CC"  
 FT Region 535..721  
 FT Region /label= B1 /note= "see CC"  
 FT Region 722..908  
 FT Region /label= B2 /note= "see CC"  
 FT Region 909..1095  
 FT Region /label= B3 /note= "see CC"  
 FT Region 1096..1159  
 FT Region /label= W /note= "see CC"  
 FT Region 1160..1179  
 FT Region /label= M /note= "see CC"  
 FT Region 1180..1185  
 FT Region /note= "charged C-terminal"

XX PD 30-APR-1992.  
 XX PR 22-OCT-1991; 91IWO-SE00207.  
 XX PA (ALFA ) ALFA LAVAL AGRI INT AB.  
 XX PI Guss BM, Hook M, Jonsson H, Lindberg KM, Patti J, Signaes LC;  
 PI Switalski LM;  
 XX DR WPI; 1992-167099/20.  
 XX DR N-PSDB; Q24123.

PS Disclosure: Fig 2; 40pp; English.

PT Hybrid DNA molecule encoding *S.aureus* collagen binding protein -  
 PT protein is expressed in *E.coli* and used for diagnosis e.g. of  
 PT septic arthritis

XX PT partially homologous p16 and cCOLRA inserts) comprises a structure  
 CC resembling a signal sequence. Following this region, a region  
 CC called A is found followed by a repetitive stretch of 187 amino  
 CC acids called B1, B2 and B3. Directly following these regions there  
 CC is a region called W which consists of a repetitive, hydrophilic  
 CC structure contg. several proline residues. This region is thought  
 CC to mediate the binding of the protein to the cell wall. The amino  
 CC acid sequence nearest to the C-terminal end consists of a long  
 CC stretch of hydrophobic residues followed by some charged amino acids  
 CC This region is called M.  
 CC The CBP can be used for immunisation pref. in combination with a  
 CC fusion protein, e.g. for vaccination of ruminants against mastitis  
 CC caused by *staphylococcal* infections. It can also be used to block  
 CC infection in an open skin wound, e.g. for blocking protein receptors  
 CC or by immunisation. In the latter, the host produces specific  
 CC antibodies which block the adherence of the bacterial strains to  
 CC damaged tissue. This treatment can be used for septic, thritis  
 CC and tissue damage of e.g. skin, connective tissue, and mucous  
 CC membranes. Dosage for immunisation is 0.5-5 microg CBP/kg; for  
 CC topical admin. the protein is used at a concn. of 25-250 microg/ml.  
 XX SQ sequence 1185 AA;

Query Match 3..78; Score 146; DB 13; Length 1185;  
 Best Local Similarity 19.28; Pred: No. 0.05B; Gaps 39;  
 Matches 152; Conservative 109; Mismatches 298; Indels 234; Gaps 39;

QY 98 LEGRSY-----QVCFNLUK-----KAFPLGSDSSVKK-W----- 126  
 Db 395 ieapryptfkdkkeyptfmkdtdnqgyfttienakaietkdvsaqvwqegtqkvkptiy 454  
 QY 127 --YKKHDGIST-----KFEDVAMSRPTIGDEL--NQKLRAMVY----- 160  
 Db 455 fklkyqddnqntpdkaeikked-gtktkvwsnlpndkngkaikykvkernagged 512  
 QY 161 --NSIPQNANGIM--EGLUPLNAIRVTOAVWYSDNAPISNDESFKRESESNLVSTS 215  
 Db 513 ttpgytktkengivvntekpiettsisgekwvdakdnqdgkrpe-----vsvn 562  
 QY 216 QLSLMRQALKLQDNLNATKMPQVPPDFQLSLISRESEDKDK-----YNGQYQNLIS 267  
 Db 563 llangekvr-ktldvtsetnwkyefd----ipkydegkkleytvtedhvkdytdin 614  
 QY 268 GGLVPTKPPPG-----DPPMPNPQPTQSVLIRKYAIGDYSKJLEGATLQLRGD 317  
 Db 615 gtti-tkypqgetsatvtrnwdnnnqgkptekvleyqdgkat---gkcatlnes 669  
 QY 318 NVNSFOARVFFSSNDIGERILSDDGTYTTLNLSPGYI-----AEPITF 362  
 Db 670 nwwtntwtgldekakqgqvk----ytveeltkvkgqyvthvddndmgnlivtqkypett 724

PN W09207002-A.



Db 709 r-etefvfegnnfnlefqnaelkgqsgskidettsfkqkkiwkdtaenrpqaiqvq 767  
Qy 566 FF----IPNNKQYQSLJGTQHPE-----DLV-----D 589  
Db 768 lyadgravegqkfigsgnewsfeknlkyngtjndijsvkeytvptydyvtsand 827  
Qy 590 IIRMEDKKEVI-----PVTHNLTRKTVNGLAGRTKDFHFEIE---IKNNKOBLLS 638  
Db 828 ii-ntkrevitqggkleetiplesgasg--gtttvedsrpvotlsglisseqqsgd 883  
Qy 639 QPVKTDK-TNLFK---DGK-----ATINIKHGESTJLQG-----LPBQSYL 677  
Db 884 mtiieedsaathikfskrdrigkelaqtatmelrdssgtistwisdqgvkdflympqytf- 942  
Qy 678 VKEIDSECKV---KVNSOEVANATVSKTGITSDETLAFENKEPVVPTG---VDQ 727  
Db 943 vetaapdgxelataititvned--ggvtngkatzgthimvdaykptksgqvldiee 1000  
Qy 728 KI 729  
Db 1001 ki 1002

Search completed: June 7, 2001, 00:17:04  
Job time: 2962 sec

